

>LGR4 nucleotide sequence (SEQ ID NO:01)

ATGCCGGGGCCCGCTAGGGCTGCTCTGCTTCCTCGCCCTGGGGCTGCTCGGCTCGGCCGGGGCCAGCGGCGCGGCGCCGCT
 CTCTGCGGGCGCCCTGCAGCTGCGACGGCGACCGTTCGGGTGGACTGCTCCGAAAGGGGTGACGGCCGTACCGGAGGGT
 CTCAGCGCCTTACCCCAAGCACTGGATATCAGTATGAACAATATCACCCAGTTACCAGAAGATGCATTTAAGAGTTTCCCA
 TTTCTAGAGGAGCTACAACCTGGCTGGTAACGACCTTTCTCTTATCCATCCAAAAGCCTTGTCTGGGCTGAAAGAAGCTCAA
 GTCCTAACACTCCAGAATAATCAGTTGAGAACAGTGGCCAGTGAAGCCATTACGGGACTGAGTGCTTTGCAGTCTTTACGC
 TTAGATGCCAACCATTATTACCTCAGTCCCGGAGGACAGTTTGAAGGGCTTGTCCAGTTACGCCATCTGTGGCTGGATGAC
 AACAGCTTGACGGAAGTGCCCGTGCCTCCCTCAGCAACCTGCCAACCTGCAGGCGCTGACCTTGGCTCTCAACAACATC
 TCAAGCATCCCTGACTTCGCTTTCACCAACCTTTCAAGCTTGGTGGTTCTGCATCTGCATAACAATAAAATTTAAAGCCTC
 AGTCAACACTGTTTTGATGGACTAGATAACCTGGAAACCTTGGACTTGAATTACAATTACTTGGATGAGTTTCTCAGGC
 ATTAAAGCCCTTCCCAGCCTTAAAGAGCTGGGATTTACAGTAATTCTATTTCTGTTATTCTCTGATGGAGCATTTGGTGGT
 AATCCACTGCTAAGAAGTATTCAATTTGTATGATAATCCTCTGCTTTTGTGGGAACTCAGCATTTTCAACACTGTCTGAT
 CTGCATTGCTTAGTCATTCGTGGTGCAAGCCTGGTGACAGTGGTTCCCAATCTGACCGAACTGCCATTTGGAGAGTCTA
 ACCTTGACAGGGACAAAAATAAGCAGCATACCTGATGATCTGTGCCAAAACAAAAGATGCTGAGGACTCTGGACTTATCT
 TATAACAATATAAGAGACCTTCCAAGTTTTAATGGTTGTCGTGCATTGGAAGAAATTTCAATGCAGCGTAATCAAATCTCC
 CTAATAAAGGAAAATACTTTTCAAGGCCTAACATCTCTAAGGATTCTAGATCTGAGTAGAAACCTGATCCGTGAAATTCAC
 AGTGGAGCTTTTGCAGAGCTTGGGACAATTACTAACCTGGATGTAAGTTTCAATGAATTAACCTTCAATTTCTACGGAAGGC
 CTAATGGGCTCAATCAACTAAAGCTTGTGGGTAACCTCAAGCTGAAAGACGCTTGGCAGCCAGAGACTTTGCTAATCTC
 AGGTCTCTATCAGTACCATATGCTTATCAGTGTGTGCATTTTGGGGGTGTGACTCTTTATGCAATTAACACAGAAGAT
 AACAGCCCCCAAGAACACAGTGTGACAAAAGAGAAAGGTGCTACAGATGCAGCAAATGTCACCAGCACTGCTGAGAAGCAA
 GAACATAGCCAAATAATTATCCACTGTACACCTTCAACAGGTGCTTTCAAGCCCTGTGAATATTTACTGGGAAGCTGGATG
 ATTCGCCTTACAGTGTGGTTCATTTTCTGGTGCCTTGCTTTTCAACCTGCTTGTCTATTTTAACAGTGTGTGCGTCTTGT
 TCATCACTGCCTGCCTCCAAACTCTTCATAGGCTTGATTTCTGTGTCTAAGTACTCATGGGCATCTATACTGGCATCCTT
 ACTTTTCTTGATGCTGTGTCTTGGGGCCGATTTGCCGAATTTGGCATTGTGGTGGGAACTGGCAGCGGCTGCAAGGTAGCC
 GGTCTCTGGCAGTCTTCTCCTCAGAGAGCGCTGTATTCCTATTAACACTGGCAGCTGTGGAAAGAAGCGTATTGTCAAAG
 GATTGTGATGAACACGGAAGAGCAGTCACCTCAGACAGTCCAGGTGGCCGCCCTCTTAGCTTTGCTGGGTGCCGAGTG
 GCAGGCTGCTTCCCCCTTTTCCACGGAGGGCAATATTCTGCATCGCCCTTGTGTTTGGCGTTTCTACAGGAGAAACCCCA
 TCGTTAGGATTCACTGTGACCTTAGTGCTATTAAACTCACTGGCATTTTTACTAATGGCCATTATCTACACTAACTATAC
 TGCAACTTAGAGAAGGAGGACCTGTGCGAAAACCTCCAGTCTAGCGTGATTAAGCACGTTGCCTGGCTCATCTTCACAAAC
 TGCATCTTCTTCTGCCCTGTTGCATTTTCTCATTTGCACCATTTGATCACGGCAATCTCCATCAGCCCCGAGATAATGAAG
 TCTGTTACACTGATATTCTTCCCGTTGCCTGCTTGCCTGAATCCGGTCTGTATGTTTCTTCAACCCAAAGTTTAAAGAA
 GACTGGAAGCTACTGAAGCGCGTGTACCAGGAAACACGGATCTGTTTCAGTTTCCATCAGCAGCCAAGGCGGTTGTGGG
 GAACAGGATTTCTACTATGACTGTGGCATGTATCCCACTTGACAGGGTAACCTGACTGTCTGTGACTGCTGTGAGTCATTT
 CTTTTGACAAAACAGTATCATGCAAACACTTAATAAAATCGCACAGTTGTCCTGTATTGACAGCGGCCTCTTGCCAGAGG
 CCAGAGGCCCTACTGGTCTGATTGTGGTACACAGTCAGCCCATTTCTGACTATGCAGATGAAGAAGATTCTTTGTCTCAGAC
 AGCTCTGACCAGGTGCAGGCCCTGTGGACGAGCCTGCTTCTACCAGAGTCGTGGATTCCCTCTGGTGCCTATGCTTACAAT
 CTACAGAGAGTCAGAGACTGA

>LGR4 amino acid sequence (SEQ ID NO:02)

MPGPLGLLCFLALGLLGSAGPSGAAPPLCAAPCSCDGD RRVD CSGKGLTAVPEGLSAFTQALDISMNNITQLPEDAFKSF
 FLEELQLAGNDLSLIHPKALSGLKEKVLTLQNNQLRTVPSEAIHGLSALQSLRLDANHITSVPEDSFEGLVQLRHLWLD
 NSLTEVPVRPLSNLPTLQALTLALNNISSIPDFAFTNLSSLVVLHLHNNKIKSLSQHCFDGLDNLETLDLNNYLDEFQQA
 IKALPSLKELGFHSNSISVIPDGAFGGNPLLRITIHLYDNPLSFVGNSAFHNLSDLHCLVIRGASLVQWFPNLTGTVHLESL
 TLTGTKISSIPDDLQCNQKMLRITLDLSYNNIRDLPSFNGCRAL E EISLQRNQISLIKENTFQGLTSLRILDLSRNLIREIH
 SGAFAKLGTITNLDVSFNELT SFPT E GLNGLNQLKLVGNFKLKDALAARDFANLRSLSVPYAYQCCAFWGCDSLCKLNTED
 NSPQEH SVTKEGATDAANVTSTAENEHSQIIHCTPSTGAFKPCEYLLGSWMIRLTWVFIFLVALLFNLLVILTVFASC
 SSLPASKLFI GLISVSNLLMGIYTGILTFDAVSWGRFAEFGIWWETGSGCKVAGSLAVFSSES AVFLLTLAVERS VFAK
 DLMKHGKSSHLRQFQVAALLALLGA AVAGCFPLFHGGQYSASPLCLFPPTGETPSLGFTVTLVLLNSLAFLLMAI IYTKLY
 CNLEKEDLSENSQSSVIKHVAWLIFTNCIFFCPVAFSFAPLIT AISPEIMKSVTLIFFPLPACLNPVLYVFFNPKFKE
 DWKLLKRRVTRKHG SVSVSISQGGCGEQDFYDCGMYSHLQGNLTVCDCESFLLTKPVSKHLIKSHSCPVLTAA SCQR
 PEAYWSDCGTQSAHSDYADEEDSFVSDSSDQVQACGRACFYQSRGFPLVRYAYNLQVRD

FIG. 1

>Nucleotide sequence of LGR5 (total 2082 nucleotides) (SEQ ID NO:03)

CTACATCTCCATAACAATAGAATCCACTCCCCTGGGAAAGAAATGCTTTGATGGGCTCCACAGCCTAGAGACTTTAGATTTA
AATTACAATAACCTTGATGAATCCCCACTGCAATTAGGACACTCTCCAACCTAAAGGAACTAGGATTTATAGCAACAAT
ATCAGGTCGATACCTGAGAAAGCATTGTAGGCAACCCCTTCTTATTACAATACATTTCTATGACAATCCCATCCAATTT
GTTGGGAGATCTGCTTTTCAACATTTACCTGAACTAAGAACACTGACTCTGAATGGTGCCTCACAAATAACTGAATTTCTT
GATTTAACTGGAAGCTGCAAACCTGGAGAGTCTGACTTTAACTGGAGCACAGATCTCATCTCTTCTCAAACCGTCTGCAAT
CAGTTACCTAATCTCCAAGTGCTAGATCTGTCTTACAACCTATTAGAAGATTTACCCAGTTTTTCAGTCTGCCAAAAGCTT
CAGAAAATTGACCTAAGACATAATGAAATCTACGAAATTAAAGTTGACACTTTCCAGCAGTTGCTTAGCCTCCGATCGCTG
AATTTGGCTTGGAACAAAATTGCTATTATTCACCCCAATGCATTTTCCACTTTGCCATCCCTAATAAAGCTGGACCTATCG
TCCAACCTCCTGTCGCTCTTTTCTATAACTGGGTACATGGTTTAACTCACTTAAATTAACAGGAAATCATGCCTTACAG
AGCTGGATATCATCTGAAAACCTTTCCAGAACTCAAGGTATAGAAATGCCTTATGCTTACCAGTGCTGTGCAATTTGGAGTG
TGTGAGAATGCCTATAAGATTTCTAATCAATGGAATAAAGGTGACAACAGCAGTATGGACGACCTTCATAAGAAAGATGCT
GGAATGTTTTCAGGCTCAAGATGAACGTGACCTTGAAGATTTCTGCTTGACTTTGAGGAAGACCTGAAAGCCCTTCATTCA
GTGCAGTGTTTACCTTCCCCAGGCCCCCTTCAAACCCCTGTGAACACCTGCTTGATGGCTGGCTGATCAGAATTGGAGTGTTG
ACCATAGCAGTTCTGGCACTTACTTGTAATGCTTTGGTGACTTCAACAGTTTTTCAGATCCCCCTCTGTACATTTCCCCCATT
AAACTGTTAATTGGGGTCATCGCAGCAGTGAACATGCTCACGGGAGTCTCCAGTGCCGTGCTGGCTGGTGTGGATGCGTTC
ACTTTTGGCAGCTTTGCACGACATGGTGCCTGGTGGGAGAATGGGGTTGGTTGCCATGTCAATTGGTTTTTTGTCCATTTTT
GCTTCAGAATCATCTGTTTTCTGCTTACTCTGGCAGCCCTGGAGCGTGGGTTCTCTGTGAAATATTCTGCAAAATTTGAA
ACGAAAGCTCCATTTTCTAGCCTGAAAGTAATCATTTTGTCTGTGCCCTGCTGGCCTTGACCATGGCCGAGTTCCCCCTG
CTGGGTGGCAGCAAGTATGGCGCCTCCCCCTCTCTGCCTGCCTTTGGCTTTTGGGGAGCCGAGCACCATGGGCTACATGGTC
GCTCTCATCTTGCTCAATTCCTTTGCTTCTCTCATGATGACCATTGCCTACACCAAGCTCTACTGCAATTTGGACAAGGGA
GACCTGGAGAATATTTGGGACTGCTCTATGGTAAAACACATTGCCCTGTTGCTCTTACCAACTGCATCCTAAACTGCCCT
GTGGCTTTCTTGCTCTTCTCTCTTTAATAAACCTTACATTTATCAGTCCTGAAGTAATTAAGTTTATCCTTCTGGTGGTA
GTCCCACTTCTGTCATGTCTCAATCCCCTTCTCTACATCTTGTTCAATCCTCACTTTAAGGAGGATCTGGTGAGCCTGAGA
AAGCAAACCTACGTCTGGACAAGATCAAAACACCCAAGCTTGATGTCAATTAACCTCTGATGATGTGCAAAAACAGTCCTGT
GACTCAACTCAAGCCTTGTAACCTTTACCAGCTCCAGCATCACTTATGACCTGCCTCCAGTTCCGTGCCATCACCAGCT
TATCCAGTGACTGAGAGCTGCCATCTTCTCTGTGGCATTGTGCCATGTCTCTAA

>amino acid sequence of LGR5 (total 693 amino acids) (SEQ ID NO:04)

LHLHNNRIHSLGKKCFDGLHSLETLDLNNLDEFPTAIRTLSNLKELGFHSNNIRSIPEKAFVGNPSLITIHFYDNPIQF
VGRSAFQHLPELRLTLNGASQITEFPDLTG TANLES LTLTGAQISSLPQTVCNQLPNLQVLDLSYNLLEDLP SFVCQKL
QKIDLRHNEIYEIKVDTFQQLLSLRLNLAWN K I A I IHPNAFSTLPSLIKLDLSSNLLSSFPITGLHGLTHLKL TGNHALQ
SWISSENFPELKVIEMPYAYQCCAFGVCENAYKISNQWNKGDNSSMDDLHKKDAGMFAQDERDLEDFLD FEEDLKALHS
VQCSPSPGPFKPCEHLLDGWLIRIGVWTIAVLALTCNALVTSTVFRSPLYISPIKLLIGVIAAVNMLTG VSSAVLAGVDAF
TFGSFARHGAWWENGVGCHVIGFLSIFASESSVFLLLTALALERGF SVKYSAKFETKAPFSSLVKVIILLCALLALTMAAVPL
LGGSKYGASPLCLPLPFGEPTMGYMLVALILLNSLCFLMMTIAYTKLYCNLDKGDLENIWDCSMVKHIALLLFTNCILNCP
VAFLSFSSLINLTFISPEVIKFI LLVVVPLPACLNPLLYILFNPHFKEDLVSLRKQTYVWTRSKHPSLMSINSDDVEKQSC
DSTQALVTFTSSSITYDLPPSSVPSPAYPVTESCHLSSVAFVPC L

FIG. 2

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>Final LGR7 (LGR7-Long variant) full length sequence (2467 nt) (SEQ ID NO:05).

GAAAGGAGGAAAGAAAAAAGAGGAATGGAAAGAGACAGAGAAAGGAAATGGGAGTGGGAAGGAGGGAGGACTGCTTT
 GTAAGTCTAAGATTGCAGACAGAAATAGCACACAACCACTGTGAGCTGTATGCGATTACAGAAACCAAGACCAAATT
 TTGCTCACTTTTCAATTAATCAGTTGCTCAGATAGAAGGAAATGACATCTGGTTCTGTCTTCTTACATCTTAATTTT
 TGGAAATATTTTTCTCATGGGGGTGGACAGGATGTCAAGTGCTCCCTTGGCTATTTCCCTGTGGGAACATCACAA
 AGTGCTTGCCTCAGCTCCTGCACTGTAACGGTGTGGACGACTGCGGGAATCAGGCCGATGAGGACAACCTGTGGAGAC
 AACAATGGATGGTCCATGCAATTTGACAAATATTTTGGCAGTTACTACAAAATGACTTCCCAATATCCTTTTGAGGC
 AGAAACACCTGAATGTTTGGTCGGTTCTGTGCCAGTGCAATGTCTTTGCCAAGGTCTGGAGCTTGACTGTGATGAAA
 CCAATTTACGAGCTGTTCCATCGGTTTCTTCAAATGTGACTGCAATGTCACTTCAGTGGAACTTAATAAGAAAAGCTT
 CCTCCTGATTGCTTCAAGAATTATCATGATCTTCAGAAGCTGTACCTGCAAAACAATAAGATTACATCCATCTCCAT
 CTATGCTTTTCAAGGACTGAATAGCCTTACTAACTGTATCTCAGTCATAACAGAATAACCTTCTCTGAAGCCGGGTG
 TTTTGAAGATCTTCACAGACTAGAATGGCTGATAATTGAAGATAATCACCTCAGTCGAATTTCCCCACCAACATTT
 TATGGACTAAATTTCTTATTCTCTTAGTCCTGATGAATAACGTCCTCACCCTTTTACCTGATAAACCTCTCTGTCA
 ACACATGCCAAGACTACATTGGCTGGACCTTGAAGGCAACCATATCCATAATTTAAGAAAATTTGACTTTTATTTCCCT
 GCAGTAATTTAACTGTTTTAGTGATGAGGAAAAACAAATTAATCACTTAAATGAAAATACTTTTGCACCTCTCCAG
 AAATGGATGAATTGGATTTAGGAAGTAATAAGATTGAAAATCTTCCACCGCTTATATTCAAGGACCTGAAGGAGCT
 GTCACAATTGAATCTTTCTATAATCCAATCCAGAAAATTCAAGCAAACCAATTTGATTATCTTGTCAAACCTCAAGT
 CTCTCAGCCTAGAAGGGATTGAAATTTCAAATATCCAACAAAGGATGTTTAGACCTCTTATGAATCTCTCTCACATA
 TATTTTAAGAAATTCAGTACTGTGGGTATGCACCACATGTTTCGAGCTGTAAACCAAACACTGATGGAATTTTCATC
 TCTAGAGAATCTCTTGGCAAGCATTATTAGAGAGTATTTGTCTGGGTTGTATCTGCAGTTACCTGCTTTTGAAACA
 TTTTGTGCTTTGATGCGACCTTATATCAGGTCTGAGAACAAAGCTGTATGCCATGTCAATCATTTCTCTCTGCTGT
 GCCGACTGCTTAATGGGAATATATTTATTCGTGATCGGAGGCTTTGACCTAAAGTTTCGTGGAGAATACAATAAGCA
 TGCGCAGCTGTGGATGGAGAGTACTATTGTGAGCTTTGTAGGATCTTTGGCCATTCTGTCCACAGAAGTATCAGTTT
 TACTGTTAACATTTCTGACATTGGAAAAATACATCTGCATTGTCTATCCTTTTAGATGTGTGAGACCTGGAAAAATGC
 AGAACAATTACAGTTCTGATTCTCATTGGATTACTGGTTTTATAGTGGCTTTTATTCCATTGAGCAATAAGGAATT
 TTTCAAAAATACTATGGCACCAATGGAGTATGCTTCCCTCTTCATTGAGAAGATACAGAAAGTATTGGAGCCCAGA
 TTTATTAGTGGCAATTTTTCTTGGTATTAATTTGGCCGATTTATCATCATAGTTTTTTCCTATGGAAGCATGTTT
 TATAGTGTTCATCAAAGTGCCATAACAGCAACTGAAATACGGAATCAAGTTAAAAAGAGATGATCCTTGCCAAACG
 TTTTCTTTTATAGTATTTACTGATGCATTATGCTGGATACCCATTTTGTAGTGAAATTTCTTTCACTGCTTCAGG
 TAGAATATACCAGTACCATAACCTCTTGGGTAGTGATTTTATTCTGCCATTAACAGTGCTTTGAACCCAATTCTC
 TATACTCTGACCACAAGACCATTTTAAAGAAATGATTGATCGGTTTTTGGTATAACTACAGACAAAGAAAATCTATGGA
 CAGCAAAGGTCAGAAAACATATGCTCCATCATTCTGCGGTGGAAATGTGGCCACTGCAGGAGATGCCACCTGAGT
 TAATGAAGCCGGACCTTTTACATACCCCTGTGAAATGTCACTGATTTCTCAATCAACGAGACTCAATTCCTATTCA
TGA

>Final LGR7 (LGR7-long variant, total 757 amino acids)(SEQ ID NO:06)

MTSGSVFFYILIFGKYFSHGGQDVKCSLGYFPCGNITKCLPQLLHCNGVDDCGNQADEDCGDNNGWSMQFDKYFA
 SYKMTSQYPFEAETPECLVGSVPVQCLCQGLELDCDETNLRAVPSVSSNVTAMSLQWNLIRKLPPDCFKNYHDLQK
 LYLQNNKITSISIIYAFRGLNSLTCLYLSHNRITFLKPGVFEDLHRLEWLIIEDNHLRSRISPTFYGLNSLILLVLMN
 NVLTRLPLDKPLCQHMPRLHWDLEGNHIIHNLRLNLTIFISCSNLTVLVMRKNKINHLNENTFAPLQKLDELGLGSKNIE
 NLPPLIFKDLKELSQLNLSYNPIQKIQANQFDYLVKLKSLSLLEGIEISNIQORMFRPLMNLSHIYFKKFQYCGYAPH
 VRSCKPNTDGISSLENLLASIIQRVFVWVSAVTCFGNIFVICMRPYIRSENKLYAMSIIISLCCADCLMGIYLFVIG
 GFDLKFGEYNKHAQLWMESTHCQLVGLSLAILSTEVSVLLLTFLTLEKYICIVYFRCVRPGKCRITITVLILIWITG
 FIVAFIPLSNKEFFKNYYGTNGVCFPLHSEDTESIGAQIYSVAIFLGINLAAPFIIIVFSYGSMFYSVHQSAITATEI
 RNQVKKEMILAKRFFFIVFTDALCWIPFVVKFLSLLQVEIPGTITSWVIFILPINSALNPILYTLTTRPFKEMIH
 RFWYNYRQRKSMDSKGQKTYAPSFIVWEMWPLQEMPPELMKPDLFTYPCEMSLISQSTRNLNSYS*

FIG. 3

>Final LGR7 (LGR7-Short variant) full length sequence (3584 nt)(SEQ ID NO:07)

CTGCTTTGTAAGTCTAAGATTGCAGACAGAAATAGCACACAACCACTGTGAGCTGTATGCGATTTCAGAAACCAAGA
 CCAAATTTTGGCTCACTTTTCTTAATCAGTTGCTCAGATAGAAGGAAATGACATCTGGTTCTGTCTTCTTCTACATCT
 TAATTTTGGAAAATATTTTCTCATGGGGGTGGACAGGATGTCAAGTGCTCCCTTGGCTATTTCCCCTGTGGGAAC
 ATCACAAGTGCTTGCCTCAGCTCCTGCACTGTAACGGTGTGGACGACTGCGGGAATCAGGCCGATGAGGACAACCTG
 TGTGGTGGTTTTGTGCCAGTGCATGTCTTTGCCAGGTCTGGAGCTTGACTGGATGAAACCATTACAGAGTGTTCAT
 CGGTTTCTTCAAATGTGACTGCAATGTCACTTCAGTGGAACTTAATAAGAAAGCTTCTCCTGATTGCTTCAAGAAT
 TATCATGATCTTCAGAAGCTGGACCTGCAAAACAATAAGATTACATCCATCTCCATCTATGCTTTCAGAGGACTGAA
 TAGCCTTACTAAACTGTATCTCAGTCATAACAGAATAACCTTCTGAAGCCGGGTGTTTTTGAAGATCTTCACAGAC
 TAGAATGGCTGATAATTGAAGATAATCACCTCAGTCGAATTTCCCCACCAACATTTTATGGACTAAATCTCTTATT
 CTCTTAGTCTGTATGAATAACGTCTCACCCTTTTACCTGATAAACCTCTCTGTCAACACATGCCAAGACTACATTG
 GCTGGACCTTGAAGGCAACCATATCCATAATTTAAGAAATTTGACTTTTATTTCTGCAGTAATTTAACTGTTTTAG
 TGATGAGGAAAAACAAAATTAATCACTTAAATGAAAATACTTTTGACCTCTCCAGAACTGGATGAATTGGATTTA
 GGAAGTAATAAGATTGAAAATCTTCCACCGCTTATATTCAAGGACCTGAAGGAGCTGTCACAATTGAATCTTCTCTA
 TAATCCAATCCAGAAAATCAAGCAAACCAATTTGATTATCTTGTCAAACCTCAAGTCTCTCAGCCTAGAAGGGATTG
 AAATTTCAAATATCCAACAAGGATGTTTAGACCTCTTATGAATCTCTCTCACATATATTTTGAAGAAATTCAGTAC
 TGTGGGTATGCACCACATGTTTCGAGCTGTAAACCAACACTGATGGAATTTTCTCTCTAGAGAATCTCTTGGCAAG
 CATTATTTCAGAGAGTATTTGTCTGGGTGTATCTGCAGTTACCTGCTTTGGAACATTTTGTCTATTGTCATGCGAC
 CTTATATCAGGTCTGAGAACAAGCTGTATGCCATGTCAATCATTTCTCTCTGCTGTGCCGACTGCTTAATGGGAATA
 TATTTATTTCGTGATCGGAGGCTTTGACCTAAAGTTTCGTGGAGAATACAATAAGCATGCGCAGCTGTGGATGGAGAG
 TACTCATTGTGAGCTTGTAGGATCTTTGGCCATTCTGTCCACAGAAGTATCAGTTTTACTGTTAAACATTTCTGACAT
 TGGAAAATACATCTGCATTGTCTATCCTTTTAGATGTGTGAGACCTGGAAAATGCAGAACAAATTACAGTTCTGATT
 CTCATTGGATTACTGGTTTTATAGTGGCTTTTATTCCATTGAGCAATAAGGAATTTTCAAAAATACTATGGCAC
 CAATGGAGTATGCTTCCCTCTTCATTTCAGAAGATACAGAAAGTATTGGAGCCAGATTTATTTCAGTGGCAATTTTTC
 TTGGTATTAATTTGGCCGCATTTATCATCATAGTTTTTCTATGGAAGCATGTTTTATAGTGTTCATCAAAGTGCC
 ATAACAGCAACTGAAATACGGAATCAAGTTAAAAAAGAGATGATCCTTGCCAAACGTTTTTCTTTATAGTATTTAC
 TGATGCATTATGCTGGATACCCATTTTTGTAGTGAAATTTCTTTCACTGCTTCAGGTAGAAATACCAGGTACCATAA
 CCTCTTGGGTAGTGATTTTTATTCTGCCATTAAACAGTGCTTTGAACCAATTCTCTATACTCTGACCACAAGACCA
 TTTAAAGAAATGATTCATCGGTTTTGGTATAACTACAGACAAAGAAAATCTATGGACAGCAAAGGTGAGAAAACATA
 TGCTCCATCATTCTGCTGGGTGGAATGTGGCCACTGCAGGAGATGCCACCTGAGTTAATGAAGCCGGACCTTTTCA
 CATACCCCTGTGAAATGTCACTGATTTCTCAATCAACAGAGACTCAATTCCTATTTCATGACTGACTCTGAAATTCATT
 TCTTCCGACAGAGAATCTGTGGGGGTGCTTCATGAGGGATTTACTGGTATGAAAATGAATACCACAAAATTAATTTAT
 AATAATAGCTAAGATAAATATTTTACAAGGACATGAGGAAAAATAAAAATGACTAATGCTCTTACAAAGGGAAGTAA
 TTATATCAATAATGTATATATATTAGTAGACATTTTGCATAAGAAATTAAGAGAAATCTACTTCAGTAACATTCATT
 CATTTTTCTAACATGCATTTATTGAGTACCCACTACTATGTGCATAGCATTGCAATATAGTCTGGAAGTAGACAGT
 GCAGAACCTTTCAATCTGTAGATAGTGTAAATGACAAAAGACTATACAAAGTCCATCTGCAGTTCCTAGTTTAAAG
 TAGAGCTTTACCTGTCTATGTGCATCAGCAAGAATCATAGGCACTTTTAAATAAAGGTTTAAAGTTTGGAACTACTCA
 GTGTATTGTGCATCATGAAAATGTCTGACTGTTTGCAAAATAATATTCTGTTTTAAGAATCCATCTTACCTCTCTTT
 AAGTTTCCATACACTTGAGAGCCAAACACAACATTTTATTACTAAAAAGATGCTTTTGCTAGAACTCAAAAACAGCA
 CTTCTTTTGGCACTTCTCTGCCAGTTTTCTCTTTGCTTTAAATGAACATCATCATATGGAATTGGAATAGGAGAGTA
 TGAGTACGGCAGAGAAGTGGATCAGAAAACTAGAATGAGGATAAACATTTACATTAGTGGAACTCCTGAAATAAA
 TCCTTGTATTGTGAGTTAACTGATTTTCAACAAGGATGCCAAGACAAAAGGCTTTTCAACAACCGTGCTGTTTTA
 AGAACAGACCTAAGTGGTTTAAATCACCACCTTTAGATGGGTGAATGTTATGGTGTGTGAAATATCTCAGTAAAGCA
 GTTAAAGGAAAAAGAGCTGGAATGCACTGATTTCAGGAACCTTAATTTTCAGGAAGGAAAGGTCTGTATGTACACATTT
 CACTTTAAGCAGAAAATCTTTCTTCAAGAAATGACTTTACTTTCTCTTTCAGTGCAGCACGTGAGATACTAAGTT
 TTTAAGTGTGTTCTTCTCTAGTCTCTACGTTATTAGNATTTTTGCTTTTATAATGTGAAACCTTTAAGCAGGAG
 AAGAAAATGTTTTAGATAGTTTTCAAATACNCCAAAATGTTTGCAACACAAAATACTGGAATCNAACCATAATGC
 CCTTATTGAATATATAGTTGTATAGNTTTGTTCTGAAAACCC

>Final LGR7-S ORF (722 amino acids) (SEQ ID NO:08)

MTSGSVFFYILIFGKYFSHGGQDVKCSLGYFPCGNITKCLPQLLHCNGVDDCGNQADEDNVCVVLCQCMSLPGLLEL
 DWMKPFTSVPSVSSNVTAMSLQWNLIRKLPDPDFKNYHDLQKLDLQNNKITSISIIYAFRGLNSLTKLYLSHNRITFL
 KPGVFEDLHRLEWLIIEDNHLRSISPPTFYGLNSLILLVLMNVNLTPLDPKPLCQHMPRLHWDLEGNHIIHNLRLNT
 FISCSNLTVLVMRKNKINHNLNENTFAPLQKLDLDELGSNKIENLPPLIFKDLKELSQNLNSYNPIQKIQAQNFQDYLV
 KLKSLLEGIEISNIQRMFRPLMNLSHIYFKKFQYCGYAPHENRSPKPNPDGIISSLENLLASIIQRVFWVWVSATVC
 FGNIFVICMRPYIRSENKLYAMSIIISLCCADCLMGIYLFVIGGFDLKFGEYNKHAQLWMESTHCQLVGLSLAILSTE
 VSVLLLTFLTLLEKYICIVYPFRVCPGKCRITITVLILIWITGFIVAFIPLSNKEFFKNYYGTNGVCFPLHSEDTEI
 GAQIYSVAIFLGINLAAFIIVFSYGSFMFYSVHQSAITATEIRNQVKEMILAKRFFFIVFTDALCWIPFVVKFLS
 LLQVEIPGTITSWVIFILPINSALNPILYTLTTRPFKEMIHRFWYNRQRKSMDSKGQKTYAPSFIVWEMWPLQEM
 PPELMKPDFTYPCEMSLISQSTRLNSYS*

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>Alignment of LGR7-L with LGR7-S

Query=LGR7-L

Sbjct=LGR7-S

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Query: 1  MTSGSVFFYILIFGKYFSHGGGQDVKCSLGYFPCGNITKCLPQLLHCNGVDDCGNQADED 60
          MTSGSVFFYILIFGKYFSHGGGQDVKCSLGYFPCGNITKCLPQLLHCNGVDDCGNQADED
Sbjct: 1  MTSGSVFFYILIFGKYFSHGGGQDVKCSLGYFPCGNITKCLPQLLHCNGVDDCGNQADED 60

Query: 61  NCGDNNGWSMQFDKYFASYKMTSQYPFEAETPECLVGSVPVQCLCQ---GLELDCDETN 117
          NC                               V V C C      GLELD  +
Sbjct: 61  NC-----VVVLCQCMSLPGLELDWMKP- 82

Query: 118  LRAVPSVSSNVTAMSLQWNLIRKLPPDCFKNYHDLQKLYLQNNKITSISIIYAFRGLNSLT 177
          +VPSVSSNVTAMSLQWNLIRKLPPDCFKNYHDLQKL  LQNNKITSISIIYAFRGLNSLT
Sbjct: 83  FTSVPSVSSNVTAMSLQWNLIRKLPPDCFKNYHDLQKLDLQNNKITSISIIYAFRGLNSLT 142

Query: 178  KLYLSHNRITFLKPGVFEDLHRLEWLIIEDNHLSRISPPTFYGLNSLILLVLMNNVLTREL 237
          KLYLSHNRITFLKPGVFEDLHRLEWLIIEDNHLSRISPPTFYGLNSLILLVLMNNVLTREL
Sbjct: 143  KLYLSHNRITFLKPGVFEDLHRLEWLIIEDNHLSRISPPTFYGLNSLILLVLMNNVLTREL 202

Query: 238  PDKPLCQHMPRLHWLDLEGNIHNLRLNTFISCSNLTVLVMRKNKINHLNENTFAPLQKL 297
          PDKPLCQHMPRLHWLDLEGNIHNLRLNTFISCSNLTVLVMRKNKINHLNENTFAPLQKL
Sbjct: 203  PDKPLCQHMPRLHWLDLEGNIHNLRLNTFISCSNLTVLVMRKNKINHLNENTFAPLQKL 262

Query: 298  DELDLGSNKIENLPPLIFKDLKELSQNLNSYNPIQKIQANQFDYLVKLKSLSLLEGIEISN 357
          DELDLGSNKIENLPPLIFKDLKELSQNLNSYNPIQKIQANQFDYLVKLKSLSLLEGIEISN
Sbjct: 263  DELDLGSNKIENLPPLIFKDLKELSQNLNSYNPIQKIQANQFDYLVKLKSLSLLEGIEISN 322

Query: 358  IQQRMFRPLMNLSHIYFKKFQYCGYAPHVRSCKPNTDGISSLENLLASIIQRFVFWVWSA 417
          IQQRMFRPLMNLSHIYFKKFQYCGYAPHVRSCKPNTDGISSLENLLASIIQRFVFWVWSA
Sbjct: 323  IQQRMFRPLMNLSHIYFKKFQYCGYAPHVRSCKPNTDGISSLENLLASIIQRFVFWVWSA 382

Query: 418  VTCFGNIFVICMRPYIRSENKLYAMSIISLCCADCLMGIYLFVIGGFDLKFRGEYNKHAQ 477
          VTCFGNIFVICMRPYIRSENKLYAMSIISLCCADCLMGIYLFVIGGFDLKFRGEYNKHAQ
Sbjct: 383  VTCFGNIFVICMRPYIRSENKLYAMSIISLCCADCLMGIYLFVIGGFDLKFRGEYNKHAQ 442

Query: 478  LWMESTHCQLVGSLAILSTEVSLLLLTFLTLEKYICIVYPFRCVVRPGKCRITITVLILIWI 537
          LWMESTHCQLVGSLAILSTEVSLLLLTFLTLEKYICIVYPFRCVVRPGKCRITITVLILIWI
Sbjct: 443  LWMESTHCQLVGSLAILSTEVSLLLLTFLTLEKYICIVYPFRCVVRPGKCRITITVLILIWI 502

Query: 538  TGFIVAFIPLSNKEFFKNYYGTNGVCFPLHSEDTE SIGAQIYSVAIFLGINLAAFIIVF 597
          TGFIVAFIPLSNKEFFKNYYGTNGVCFPLHSEDTE SIGAQIYSVAIFLGINLAAFIIVF
Sbjct: 503  TGFIVAFIPLSNKEFFKNYYGTNGVCFPLHSEDTE SIGAQIYSVAIFLGINLAAFIIVF 562

Query: 598  SYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVFTDALCWIPFVVKFSLSLQVEI 657
          SYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVFTDALCWIPFVVKFSLSLQVEI
Sbjct: 563  SYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVFTDALCWIPFVVKFSLSLQVEI 622

Query: 658  PGTITSWVVFILPINSALNPILYTLTTRPFKEMIHRFWYNYRQRKSMSDSKGQKTYAPSF 717
          PGTITSWVVFILPINSALNPILYTLTTRPFKEMIHRFWYNYRQRKSMSDSKGQKTYAPSF
Sbjct: 623  PGTITSWVVFILPINSALNPILYTLTTRPFKEMIHRFWYNYRQRKSMSDSKGQKTYAPSF 682

Query: 718  IWVEMWPLQEMPPELMKPDLTYPCEMSLISQSTRLNSYS 757
          IWVEMWPLQEMPPELMKPDLTYPCEMSLISQSTRLNSYS
Sbjct: 683  IWVEMWPLQEMPPELMKPDLTYPCEMSLISQSTRLNSYS 722

```

FIG. 5

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FIG. 6

Signal peptide

LGR4 MPGPLGLLCFLALGLLGSAGPSGA
LGR5 MDTSRLGVLLSLPVLLQLATG
LHR MKQRFSAQLLKLKLLQLPPLPRA
FSHR MALLLVSLLAFLSLGSG
TSHR MRPADLLQLVLLLDLPRDLGG

N-flank cysteine-rich sequence

LGR4 APPL AA-P S DGDR---RVD SGKGLTAVPEGLSAFTQA
LGR5 GSSPRSGVLLRG P-TH H EPDGRMLLRVD SDLGLSELPSNLSVFTSY
LHR LREAL P-EP N VPDG--ALR-- PGPTAGLTR
FSHR HHRI H SNRVFL----- QESKVTEIPSDLPNAIE
TSHR MG SSPP E HQEED--FRVT KDIQRIPSLPPSTQT

Leucine-rich repeats


| | | | | | | | | | |
|------|--------------------------------|----------------|----|--------|---------|-----------|--------|-----------|------|
| LGR4 | DISMNNITQLPED | KSFPFLEELQLAGN | -- | SL | HPKALSG | KE | KVLTLO | -- | Q |
| LGR5 | DLSMNNISQLLPNPLPSLHFLEELRLAGNA | -- | TY | PKGA | TG | YS | KVLMLO | -- | Q |
| LHR | SLAYLPVKVIPSQ | RLNEVIKIEISQI | S- | ER | EANA | DN | LN | SEILIQ | TK - |
| FSHR | RFVLTKLRVIOKG | SGFGDLEKIEISQN | V- | EV | EADV | SN | PK | HEIRIEKAN | - |
| TSHR | KLIETHLRTIPSH | SNLPNISRIYVSI- | VT | QQLSHS | YN | SKVTHIEIR | TR | - | - |

| | | | | | | | | | | | | | | |
|------|------|----|-----|----|----|------|--------|-------|------------|-----------|------|------|----|-----|
| LGR4 | RTV- | SE | IHG | SA | QS | RLDA | H- | TSV | EDS-- | FEGVLQLRH | WLD | S-L- | EV | VR |
| LGR5 | RHV- | TE | LQN | RS | QS | RLDA | H- | SYV | P-SC- | FSGLHSLRH | WLD | A-L- | E | VQ |
| LHR | RYIE | -G | FIN | PG | KY | SIC- | TG | RKF | DVTKVFSSES | NFI- | EIC | LHI- | T | GN |
| FSHR | LYIN | -E | FQN | PN | QY | LIS- | TG | KHL | DVHK- | IHSLQKVL- | DIQ | INIH | - | ERN |
| TSHR | TYID | -D | LKE | PL | KF | GIF- | TGLKMF | DLTK- | VYSTDIFFI | EIT | PYM- | S | VN | |

| | | | | | | | | | | | | | |
|------|------|--------|----------|----|----------|----------|-------|-----|------|----|------------|------------|--------|
| LGR4 | PLSN | P-TLQA | T | AL | NISSIPDF | T | LSS | VV | H | HN | K-IKSLSQHC | D | LDN-LE |
| LGR5 | A | RS | S-ALQAMT | AL | KIHHIPDY | G | LSSWV | V | H | HN | R-IHSLGKKC | D | LHS-LE |
| LHR | A | QGMNNE | SVT | K | YG | GFEEVQSH | - | GTT | TS | E | KE | VHLEKMHNGA | R |
| FSHR | S | VG | SFESVI | W | NK | GIQEIHNC | - | GTQ | DE | N | SD | NNLEELPNDV | H |
| TSHR | A | QG | CNETLT | K | YN | GFTSVQGY | - | GTK | DAVY | NK | KYLTVIDKDA | G | VYSGPS |

| | | | | | | | | | | | |
|------|---|----|---------|----------|----|---------------|------------|-------|--------|-------|-------|
| LGR4 | T | LN | NYNLDEF | Q-AIKA | PS | KELGFHSNSISVI | D-GA | GGNPL | RTIH | - | DNPLS |
| LGR5 | T | LN | YNNLDEF | T-AIRT | SN | KELGFHSNNIRSI | E-KA | VGNPS | ITIHF- | DNPIQ | |
| LHR | T | IS | STKLQAL | SYGLESIQ | R | I-ATS-SYSLKKL | SRET | V-N-- | LEAT | T | |
| FSHR | I | IS | RTRIHSL | SYGLEN | KK | R-ARSTYN-LKKL | TLEKLVA--- | MEAS | T | ---- | |
| TSHR | L | VS | QTSVTAL | SKGLEH | KE | I-ARNTWT-LKKL | LSLS | LH--- | TRAD | S | |

| | | | | |
|------|--|--------|----|---------------------|
| LGR4 | FVGNSAFHNLSDLHCLVIRGASLVQWFPNLTGTVHLES | LT | TG | TKISSIPDDLCQNQKML |
| LGR5 | FVGRSAFQHLPELRTLTLNGASQITEFPDLTG | TANLES | LT | TGAQISSLPQTVCNQLPNL |
| LHR | ----- | | | |
| FSHR | ----- | | | |
| TSHR | ----- | | | |



| | |
|------|-------------------------------------|
| LGR4 | SGAFAKLGTITNLDVSNELTSFPTEGLNGLNQLK |
| LGR5 | PNAFSTLPSLIKLDLSSNLLSSFPITGLHGLTHLK |
| LHR | ----- |
| FSHR | ----- |
| TSHR | ----- |

| | | | |
|------|--------------------------|------|------------------------------|
| LGR4 | LVGNFKLKDALAARDFANLRSLSV | YAYQ | WGCDSLCKLNTEDNSPQEHSVTKEKGA |
| LGR5 | LTGNHALQSLISSENFPELKVIM | YAYQ | GVCENAYKISNQWNKGDNSSMDDLHKK |
| LHR | ----- | --SH | RNLPTKEQNFSSHSISENFSKQCESTVR |
| FSHR | ----- | --SH | ANWRRQISELHPICNKSILRQEVDMYT |
| TSHR | ----- | --SH | KNOKKIRGILESMLCNESSMQSLRQK |

| | | |
|------|---------------|---|
| LGR4 | TDAANVTSTAENE | HS----- |
| LGR5 | DAGMFQAQDERDL | DF----- |
| LHR | KVSNKTLYSSMLA | SE----- |
| FSHR | QTRGQRSSLAEDN | SS----- |
| TSHR | SVNALNSPLHOEY | ENLGDSIVGYKEKSKFODTHNNAHYYVFEEEOEDEIIIGFGQELKNP |

| | | | | | |
|------|--------------------------|---|------|---|----------|
| LGR4 | -----QIIHH | T | STGA | K | YLLGSWMI |
| LGR5 | -----LLDFEEDLKALHSVQ | S | SPGP | K | HLLDGWLI |
| LHR | -----LSGWDYEGFCLPKTPR | A | EPDA | N | DIMGYDFL |
| FSHR | YSRGFDMTYTEFDYDLNCSEVDVT | S | KPDA | N | DIMGYNIL |
| TSHR | OETLOAFDSHYDYICGDSMDMV | T | KSDE | N | DIMGYKFL |

TM 1

| | | | | | | | | | | |
|------|------|------|-----|-----|--------|--------|-----------|-------------------|--------------|---------------|
| LGR4 | LTV | F | FLV | LLF | LL | ILTVFA | CSS | PASKLFIGLISVSNLLM | IYTGILTFL | AVSW |
| LGR5 | IGV | T | AV | LTC | AL | TSTVFR | PLYISPIKL | IGVIAAVNMLT | VSSAVL | G AF F |
| LHR | VL I | L | NI | IMG | MT | LEVLLT | RYK | TVPRF | MCNLSFADFCM | LYLLLI S SQ K |
| FSHR | VL I | F | SI | ITG | II | LVILTT | QYK | TVPRF | MCNLAFAADLCI | IYLLLI S IH K |
| TSHR | IVV | FVSL | LLG | VF | LLILLT | HYK | NVPRF | MCNLAFAADFCM | MYLLLI S | LY H |

TM 2

TM 3

| | | | | | | | | | | | | |
|------|-----------|----|---|-----|-----|-----|---|----|----|------|-----------------|--------|
| LGR4 | GRFAEFG | W | E | S | KV | SLA | S | SA | FL | LAHV | SVFAKDLMKHGKSSH | QF |
| LGR5 | GSFARHGAW | EN | V | HVI | LSI | | | S | FL | LAA | GFSVKYSAKFET | APFSSL |
| LHR | GQYYNHA | D | Q | S | ST | FT | | L | YT | VIT | WHTITYAIHLDO | LR |
| FSHR | SQYHNYA | D | Q | A | DA | FT | | L | YT | AIT | WHTITYAMQLDC | VQ |
| TSHR | SEYYNHA | D | O | P | NT | FT | | L | YT | VIT | WYAITEFAMRLDR | IR |

FIG. 6 (CONT)

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| | <u>TM 4</u> | | | | <u>TM 5</u> | | | |
|------|-------------------|--------|--------|-------------------|-------------|------|------|--|
| LGR4 | QVAALLALLGAAVAGCF | FHGGQ | SASPL | FPTGETPSLGFTVTLVL | SL | LLMA | | |
| LGR5 | KVIILLCALLALTM AV | L G K | GASPL | LPFGEPSTMG | MVALIL | SLC | LMMT | |
| LHR | ILIMLGGWLFSSLI ML | V V N | MKVSIF | MDVETTLISQV | ILTILI | VV | FIIC | |
| FSHR | ASVMVMGWIFAFAA LF | IF I S | MKVSIF | MDIDSPLSQL | VMSLLV | VL | VVIC | |
| TSHR | CAIMVGGWVCCFLL LL | V I S | AKVSI | MDTETPLALA | IVFVLT | IV | VIVC | |

| | <u>TM 6</u> | | | | | | | |
|------|-------------|--------------------|-------------|--------|----|-------------|---------|------|
| LGR4 | II T L | CNL-EKEDLSENSQSSVI | HV W | NCIFFC | VA | FSFAPLITAIS | SPEI | |
| LGR5 | IA T L | CNL-DKGDLENIW | CSMV HI L L | NCILNC | VA | LSF | SLINLTF | SPEV |
| LHR | AC I I | FAVRNPELMATNK | TKIA KM I | DFTCMA | IS | FAI | AAFKVPL | TVTN |
| FSHR | GC IHI | LTVRNPNIVSSSS | TRIA RM M | DPLCMA | IS | FAI | ASLKVPL | TVSK |
| TSHR | CCHV I | ITVRNPQYNPGDK | TKIA RM V | DFICMA | IS | YAL | AILNKPL | TVSN |

| | <u>TM 7</u> | | | | | |
|------|-------------|-------|------|-----|-----|----------|
| LGR4 | M | SVTLI | F | LPA | L | V VF N |
| LGR5 | I | FI | LVVV | LPA | L | L IL N |
| LHR | S | VL | VL | Y | INS | A F AI T |
| FSHR | A | IL | VL | H | INS | A F AI T |
| TSHR | S | IL | VL | Y | LNS | A F AI T |

C-terminal tail

| | |
|------|---|
| LGR4 | PK KE WKL KRRVTRKHGSVSVSISSQGGCGEQDFYDCGMYSHLQGNLTVCDCCESFL |
| LGR5 | PH KE LVS RKQTYVWTRSKHPSLMSINSDDVEKQSCDSTQALVTFTSSSITYDLPPSS |
| LHR | KT QR FFL LSKFGCCKRRRAELYRRKDFSAYTSNCKNGFTGSNKPSQSTLKLSTLHCQG |
| FSHR | KN RR FFI LSKCGCYEMQAQIYRTETSSTVHNTHPRNGHCSSAPRVTNGSTYILVPLS |
| TSHR | KA QR VFI LSKFGICKRQAQAYRGQRVPPKNSTD IQVQKVTHDMRQGLHNMEDVYELI |

| | |
|------|---|
| LGR4 | LTKPVSCKHLIKSHSFCPVLTAASCQRPEAYWSDCGTQSAHSDYADEEDSFVSDSSDQVQA |
| LGR5 | VPSPAYPVTESCHLSSVAFVPCL |
| LHR | TALLDKTRYTEC |
| FSHR | HLAQN |
| TSHR | ENSHLTPKKQGQISEEYMQTVL |

| | |
|------|---------------------------|
| LGR4 | CGRACFYQSRGFPLVRYAYNLQVRD |
|------|---------------------------|

FIG. 6 (CONT)